

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.7349 Seconds

(Without alignments)
837,928 Million cell updates/sec

Title: US-09-622-613b-26

Perfect score: 606

Sequence: 1 NSMWATFOOKHIIIMPICN.....ICVKCENQYFVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PTR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Result No. Query Match Length DB ID

Result No.	Score	Match	Length	DB ID	Description
1	586.5	96.8	111	2	A27121
2	450	74.3	111	1	JX0120
3	369	60.9	111	2	JX0085
4	272.5	45.0	104	2	A39035
5	135.5	22.4	124	1	NRWHR
6	135.5	22.4	145	1	A35932
7	133.5	22.0	167	2	S20066
8	132.5	21.9	124	1	NRPG
9	126.5	20.9	119	2	S41111
10	122.5	20.2	124	1	NRPRH
11	122	20.1	122	1	NRKGR
12	120.5	19.9	128	1	NRKV
13	120.5	19.9	149	1	NRMS
14	119.5	19.9	123	1	A43825
15	118.5	19.6	128	1	NRGPB
16	117.5	19.4	128	1	NRHO
17	116.5	19.2	124	1	NRKM
18	116.5	19.2	124	1	NRKM
19	116.5	19.2	124	1	NRKM
20	116.5	19.2	124	1	NRKM
21	114.5	18.9	124	2	S08549
22	114	18.8	125	1	A32474
23	113.5	18.7	124	1	NRDEN
24	113.5	18.7	125	1	E43825
25	113	18.6	147	1	NRHAG
26	112.5	18.6	124	1	NRGF
27	112.5	18.6	124	1	NRDEO
28	111.5	18.4	130	2	S22808
29	110.5	18.2	124	1	NRBOB

SUMMARIES

ALIGNMENTS

Query Match	Score	DB 1	Length	DB 2	Score	DB 1	Length	DB 2	Score	DB 1	Length	DB 2
30	110.5	18.2	124	1	NRWB	pancreatic ribonuc						
31	110.5	18.2	124	1	NREKN	pancreatic ribonuc						
32	110.5	18.2	124	2	S07141	pancreatic ribonuc						
33	110.5	18.2	124	2	JC5560	pancreatic ribonuc						
34	110.5	18.2	150	1	NRBO	pancreatic ribonuc						
35	110.5	18.2	158	2	I61900	pancreatic ribonuc						
36	109.5	18.1	124	1	NRSH	pancreatic ribonuc						
37	108.5	17.9	119	2	JX0115	pancreatic ribonuc						
38	108.5	17.9	124	1	NRCH	pancreatic ribonuc						
39	108.5	17.9	152	1	NRRT	pancreatic ribonuc						
40	106.5	17.6	124	1	NRHP	pancreatic ribonuc						
41	106.5	17.6	125	4	A47498	pancreatic ribonuc						
42	106.5	17.6	150	1	NRBOS	pancreatic ribonuc						
43	104.5	17.2	124	1	NRGN	pancreatic ribonuc						
44	104.5	17.2	124	1	NRDF	pancreatic ribonuc						
45	104	17.2	125	2	S04503	pancreatic ribonuc						

RESULT 1

A27121
ribonuclease-related stalic acid-binding lectin - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C:Accession: A27121
R:Tilani, K., Takio, K., Kuwada, M., Nitta, K., Sakakibara, F., Kawachi, H., Takayan
Biochemistry 26, 2189-2194, 1987
A:Title: Amino acid sequence of stalic acid-binding lectin from frog (Rana catesbeiana)
A:Reference number: A27121; MUID:87299649; PMID:3304421
A:Accession: A27121
A:Molecule type: protein
A:Residues: 1-111 <TT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin

Query Match 96.8% Score 586.5; DB 2: Length 111;
Best Local Similarity 99.1%; Pred. No. 2, 6e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	3	NRWATFOOKHIIIMPICN	NTIMDNIIYVGQCKRVMTFIISATYKATGVINNVL	61
Db	2	NSMWATFOOKHIIIMPICN	NTIMDNIIYVGQCKRVMTFIISATYKATGVINNVL	61
Qy	62	STTFQOLNCTRTSITPRCPYSSRTETNYICVCEMOYFHFAGIGRCP	111	
Db	62	STTFQOLNCTRTSITPRCPYSSRTETNYICVCEMOYFHFAGIGRCP	111	

RESULT 2

JX0120
ribonuclease-related stalic acid-binding lectin - Japanese frog
C:Species: Rana japonica (Japanese frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JX0120
R:Kamita, Y., Oyama, F., Oyama, R., Sakakibara, F., Nitta, K., Kawachi, H., Takeyana
J. Biochem. 108, 139-143, 1990
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A:Reference number: JX0120; MUID:91035319; PMID:2229005
A:Accession: JX0120
A:Molecule type: protein
A:Residues: 1-111 <KAM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin; pyroglyutamic acid
F:1/Modified site: pyroglutamic acid (Gln) #status experimental
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.3% Score 450; DB 1: Length 111;
Best Local Similarity 78.2%; Pred. No. 9, 2e-38;
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

OY 3 NMAFQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 60
 DB 2 NMAFQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 61
 OY 61 LSTTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQVPHVAGIGRC 110
 DB 62 LSTTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQVPHVAGIGRC 111

RESULT 3

JX0085
 pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
 C:Species: Rana catesbeiana (bullfrog)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
 C:Accession: JX0085
 R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
 J. Biochem. 106, 729-735, 1989
 A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
 A:Reference number: JX0085; MUID:90130374; PMID:2613682
 A:Accession: JX0085
 A:Molecule type: protein
 A:Residues: 1-111 <NTT>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: hydrolase; pyroglyutamic acid
 F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F:10/35,104/Active site: His, Lys, His #status predicted
 F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 60.9% Score 369; DB 2; Length 111;
 Best Local Similarity 65.5%; Pred. No. 1e-29;
 Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

OY 3 NMAFQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 60
 DB 2 NMAFQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 61
 OY 61 LSTTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQVPHVAGIGRC 110
 DB 62 LSTTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQVPHVAGIGRC 111

RESULT 4

A39035
 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
 C:Species: Rana pipiens (northern leopard frog)
 C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
 C:Accession: A39035
 R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
 J. Biol. Chem. 266, 245-251, 1991
 A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
 A:Reference number: A39035; MUID:91093131; PMID:1985896
 A:Accession: A39035
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-104 <ARD>
 C:Superfamily: pancreatic ribonuclease

Query Match 45.0% Score 272.5; DB 2; Length 104;
 Best Local Similarity 49.1%; Pred. No. 3.6e-20;
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

OY 3 NMAFQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 60
 DB 2 NMAFQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 61
 OY 61 LSTTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQVPHVAGIGRC 110
 DB 58 LSTTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQVPHVAGIGRC 104

RESULT 5

NRMHK
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale

N:Alternate names: RNase 1; RNase A
 C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
 C:Accession: A00818
 R:Emmens, M.; Wellings, G.W.; Beintema, J.J.
 Biochem. J. 157, 317-323, 1976
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea
 A:Reference number: A00818; MUID:76277855; PMID:962870
 A:Accession: A00818
 A:Molecule type: protein
 A:Residues: 1-124 <EMM>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12/41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (asn) (covalent) (partial) #status experimental

Query Match 22.4% Score 135.5; DB 1; Length 124;
 Best Local Similarity 33.3%; Pred. No. 1.7e-06;
 Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

OY 7 FQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 60
 DB 8 FQOKHIIIMP-IICNTIMDNIIYVGGCKRVNTFISSATVKAICTGY-INMNV 61
 OY 61 LSTTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQVPHVAGIGRC 110
 DB 64 LCKKGRNCTCYESNTHIITDCRGTGSSSKYINCAVTKQKHHIIVACENGPRVPHF 120

RESULT 6

A35932
 angiotensin precursor - mouse
 N:Alternate names: angiotensin factor
 N:Contains: ribonuclease (EC 3.1.27.-)
 C:Species: Mus musculus (house mouse)
 C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
 C:Accession: A35932
 R:Bond, M.D.; Vaillee, B.L.
 Biochem. Biophys. Res. Commun. 171, 988-995, 1990
 A:Title: Isolation and sequencing of mouse angiotensin DNA.
 A:Reference number: A35932; MUID:91025023; PMID:2222458
 A:Accession: A35932
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-145 <BON>
 A:Cross-references: GB:U22516; NID:9726325; PIDN:AAA91366.1; PID:9726326
 C:Genetics:
 A:Introns: #status absent
 C:Function:
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissu
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglyutamic acid
 F:1/24/Domain: signal sequence #status predicted <SIG>
 F:25-145/Product: angiotensin #status predicted <MAT>
 F:25/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predic
 F:37,64,137/Active site: His, Lys, His #status predicted
 F:50-104,63-115,61-130/Disulfide bonds: #status predicted

Query Match 22.4% Score 135.5; DB 1; Length 145;
 Best Local Similarity 39.5%; Pred. No. 2e-06;
 Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

OY 34 CKRVNFISSATVKAICTGY-INMNV-LSTTRFOLNCTRTSITPR-PPYSSRTE 88
 DB 63 CKRVNFISSATVKAICTGY-INMNV-LSTTRFOLNCTRTSITPR-PPYSSRTE 89
 OY 89 TNYICVCKENQVPHF 104
 DB 123 FRHVIACENGPRVPHF 138

RESULT 7

S20066
pancreatic-type ribonuclease (EC 3.1.27.5) Brb precursor, brain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C:Accession: S20066; JX0056
R:Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri, Nucleic Acids Res. 19, 6469-6474, 1991
A:Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A:Reference number: S20066; MUID:92093604; PMID:1754384
A:Accession: S20066
A:Molecule type: DNA
A:Residues: 1-167 <SAS>
A:Cross-references: EMBL:X59767; NID:9150; PIDN:CAA42439.1; PID:9151
R:Matanah, H.; Katch, H.; Ishii, M.; Komoda, Y.; Sando, A.; Takizawa, Y.; Ogi, K.; Iri
J. Biochem. 104, 939-945, 1988
A:Title: Primary structure of a ribonuclease from bovine brain.
A:Reference number: JX0056; MUID:89214015; PMID:3243767
A:Accession: JX0056
A:Molecule type: protein
A:Residues: 27-154, 'S', 156-166 <MAT>
A:Experimental source: brain
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase
F:38,67,145/Active site: His, Lys, His #status predicted
F:52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:155/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 22.0%; Score 133.5; DB 2; Length 167;
Best local Similarity 31.4%; Pred. No. 3.7e-06;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

QY 5 ATFOCKHI-----INPIICNTIMDNIIYVGCKRVNFIISATVKAICTGVINM 58
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 32 AKRICHMDSGSSSSSNPCNOMKRR-RRTGRCKPVPFVHESLDYKAVCS--QK 87
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 59 NVL-----STTFOLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHFA 105
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 88 NITCKNGHPKCYOSKSMSTITDREITGSSKYPNCATYTSOKYITVACGPNPVPHFD 147
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 106 G 106
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 148 G 148

RESULT 8
NRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
N:Alternate names: RNase 1; RNase A
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1981 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A92071; A91391; A00816
R:Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A:Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A:Reference number: A92071; MUID:70104197; PMID:5460946
A:Accession: A92071
A:Molecule type: protein
A:Residues: 1, 'Q', 3-124 <JAC>
R:Wierenga, R.K.; Hultzinga, J.D.; Gaaststra, W.; Wellling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A:Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A:Reference number: A91391
A:Accession: A91391
A:Molecule type: protein
A:Residues: 1-124 <WIE>
R:Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A:Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A:Reference number: A92072; MUID:70104198; PMID:4904878
C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,34,119/Active site: His, Lys, His #status predicted
F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match 21.9%; Score 132.5; DB 1; Length 124;
Best local Similarity 31.6%; Pred. No. 3.5e-06;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 7 EQCKHI-----INPIICNTIMDNIIYVGCKRVNFIISATVKAICTGV-INNM 59
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 8 FOROHNDPSSSSSNSSNYCMMSRR-NMQGCKRPVNFVHESLDYKAVCSQIWNCK 66
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 60 VLSTFRPLNT-----CTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHFA 104
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 67 NGOTNCTOSNMTHITDRCROTGSSKYPNCATYTSOKYITVACGPNPVPHFD 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 9
S4111
pancreatic ribonuclease - common iguana
C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A:Reference number: S4111; MUID:94139745; PMID:8307028
A:Accession: S4111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match 20.9%; Score 126.5; DB 2; Length 119;
Best local Similarity 29.8%; Pred. No. 1.3e-05;
Matches 34; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 3 NMATFOCKHI-----INPIICNTIMDNIIYVGCKRVNFIISATVKAICTGVINM 52
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 2 DWSSFOKHIDYETSASNPAYCDLMOQR-NLNPCKCKTRTNPVHASESEIQQVCGSG 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 53 -TGVINMNVLSTFRPLNTCTRTSIT-PRCPYSSRTETNYICVKE-NQY-PVHFA 104
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 61 GTHYEDNLVDSNSESFDLTDCKNNGTAPSSCKYNGTPTGRITACENNPVPHF 114
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Antilocapra americana (pronghorn)
C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C:Accession: A00813
R:Beintema, J.J.; Gaaststra, W.; Munnikswa, J.
J. Mol. Evol. 13, 305-316, 1979
A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship b
A:Reference number: A00813; MUID:80075014; PMID:513141
A:Accession: A00813
A:Molecule type: protein
A:Residues: 1-124 <BEI>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.2%; Score 122.5; DB 1; Length 124;
Best local Similarity 30.3%; Pred. No. 3.4e-05;
Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

QY 5 ATFOCKHIINTPI-----ICNTIMDNIIYVGCKRVNFIISATVKAICTGVINM 58
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Db 6 AKERHIDNSPSSVSSNNCNOMKSR-NLTGRCRKPNTFVHESLADVOAVCS---QK 61
 59 NVL-----STTRFQNLNCTRTSTTPRP-CPYSSRTETNYICVKE-NQY-PVHF 104
 62 NVACKNGOTNCGYSYMSITDCRETGSSKRPNTVHETQAKKHIIVACEGNPIYPVPHY 120

RESULT 11

NRKRCR
 pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
 N:Alternate names: RNase A
 C:Species: Macropus rufus, Megaleia rufa (red kangaroo)
 C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
 A:Accession: A00833
 R:Gastra, W.; Wellling, G.W.; Beintema, J.J.
 Eur. J. Biochem. 86, 209-217, 1978
 A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
 A:Reference number: A00833; MUID:78190621; PMID:658039
 A:Accession: A00833
 A:Molecule type: protein
 A:Residues: 1-122 <GAA>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:11,40,117/Active site: His, Lys, His #status predicted
 F:25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
 F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.1%; Score 122; DB 1; Length 122;
 Best Local Similarity 30.7%; Pred. No. 3.8e-05;

Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

Db 7 FOOKHI-----INTPLICNTIMDNNTIYVGGCKRVTFLISSATVKAIC----- 52
 7 FORGHMDEHSTASSSVNCNLMKAR-DMTSGRCKPLNTFHEBKVADVACQENVTCK 65
 53 TGVNMMVLTSTRFQNLNCTRTSTTPRP-CPYSSRTETNYICVCE-NQY-PVHF 104
 66 NGRTNC-YKSNRSLTNCROTGASKYPCOYERSNLTQYVACQGVVPHF 118

RESULT 12

NRCU
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
 N:Alternate names: RNase 1; RNase A
 C:Species: Myocastor coypus (nutria, coypu)
 C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
 A:Accession: A00832
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
 Biochim. Biophys. Acta 453, 400-409, 1976
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
 A:Accession: A00812; MUID:77065676; PMID:995896
 A:Molecule type: protein
 A:Residues: 1-128 <VAN>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:11,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.9%; Score 120.5; DB 1; Length 128;
 Best Local Similarity 31.6%; Pred. No. 5.6e-05;

Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

Db 7 FOOKHI-----INTPLICNTIMDNNTIYVGGCKRVTFLISSATVKAICGVIMNV 60
 8 FERGHMDSRSPSTNRYCNEMKSR-NMTOGRCKPNTVHETQAKKHIIVACEGNPIYPVPHY 120
 61 L-----STTRFQNLNCTRTSTTPRP-CPYSSRTETNYICVKE-NQY-PVHF 104
 64 LCKNGOTNCGYSYMSITDCRETGSSKRPNTVHETQAKKHIIVACEGNPIYPVPHF 120

RESULT 13

NRMS
 pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
 N:Alternate names: RNase 1; RNase A
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
 A:Accession: A34090; S22598; A00830
 R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
 Mol. Biol. Evol. 7, 29-44, 1990
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mo
 A:Reference number: A34090; MUID:90136034; PMID:2259980
 A:Accession: A34090
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-149 <SCCH>

A:Cross-references: CB:M27814; NID:g200762; PIDN:AAA0060.1; PID:g200763
 R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koepf, D.; Weisler, M.H.
 Nucleic Acids Res. 19, 6935-6941, 1991
 A:Title: Isolation of the murine ribonuclease gene R1b-1: structure and tissue specif
 A:Reference number: S22598; MUID:92107684; PMID:1840677
 A:Accession: S22598

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-149 <SAM>
 A:Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
 R:Lenstra, J.A.; Beintema, J.J.
 Eur. J. Biochem. 98, 399-408, 1979

A:Title: The amino acid sequence of mouse pancreatic ribonuclease.

A:Reference number: A00830; MUID:80024269; PMID:556267

A:Accession: A00830
 A:Molecule type: protein
 A:Residues: 26-149 <LEN>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-149/Product: pancreatic ribonuclease #status predicted <MAT>
 F:37,66,144/Active site: His, Lys, His #status predicted
 F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
 F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.9%; Score 120.5; DB 1; Length 149;
 Best Local Similarity 30.8%; Pred. No. 6.5e-05;

Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

Db 7 FOOKHI-----INTPLICNTIMDNNTIYVGGCKRVTFLISSATVKAICGVIMNV 60
 33 FORGHMDDSSINSPIYCNOMKRR-DMTNGSKRPNTVHETQAKKHIIVACEGNPIYPVPHF 145
 61 L-----STTRFQNLNCTRTSTTPRP-CPYSSRTETNYICVKE-NQY-PVHF 104
 89 TCKNRKNCYKSSALHITDCHLKGNSKYPNCQYKTYQYQKHIIVACEGNPIYPVPHF 145

RESULT 14

A43825
 angiotensin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: S29834; A43825
 R:Bond, M.D.; Strydom, D.J.; Vallée, B.L.
 Biochim. Biophys. Acta 1162, 177-186, 1993
 A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discer
 A:Reference number: S29833; MUID:93192291; PMID:8448182
 A:Accession: S29834
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-123 <BON>
 A:Note: this sequence was submitted to the Protein Sequence Database, December 1992
 C:Superfamily: pancreatic ribonuclease

Query Match 19.7%; Score 119.5; DB 1; Length 123;
 Best Local Similarity 39.5%; Pred. No. 6.7e-05;
 Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

[illegible]

RESULT 15

pancreatic ribonuclease (EC 3.1.27.5) P - guinea pig (tentative sequence)
N:Alternate names: RNase IB
C:Species: Cavia porcellus (guinea pig)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
A:Accession: A00826
R:van den Berg, A., van den Heide-Timmer, L.: Hofsteenge, J.: Gastra, W.: Beintema, J. J. Eur. J. Biochem. 75, 91-100, 1977
A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure
A:Reference number: A91247; MUID:77185023; PMID:862624
A:Accession: A00826
A:Molecule type: protein
A:Residues: 1-128 <VAN>
A:Note: 64-Pro was also found
A:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:21.34/Binding site: carbohydrate (asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

	Query Match	19.6%	Score 118.5	DB 1:	Length 128:
	Best Local Similarity	31.6%:	Pred. No. 8.8e-05:		
	Matches 37:	Conservative 14:	Mismatches 43:	Indels 23:	Gaps 6:
QY	7 FOKKHI-----IMPIICNTIMDNINIIYVGCGCKRVMTFLISSATFKAICTGIVNNV 60				
Dd	8 FQRGHMDEGGSPSSNNSNCNVMMIIR-NMTQGRCRCPVMTFHESLADAOAVC---FOKNV 63				
QY	61 L-----STRPOLNCTRTSTIPRP-CPYSSRFETNYICVKENCQ--YPVHF 104				
Dd	64 LCRKKQCINCIOYSRMRIIDCRRVTSSSKAFPCSRMSAQAKSIIVACGCDPVVPVHF 120				

Search completed: June 25, 2003, 14:58:07
Job time : 13.7349 secs

